4446

(FILE 'USPAT' ENTERED AT 12:16:31 ON 17 DEC 96)
L1 3656 S (CLEAVASE(W)BN) OR TAC OR TTH OR (EXO III) OR RAD1/RAD10
L2 311 S (7(W)DEAZA(W)DATP) OR (7(W)DEAZA(W)DGTP) OR DUTP
L3 16310 S CAMPYLOBACTER? OR ESCHERICHIA OR MYCOBACTER? OR SALMONEL
LA
=> s l1 and l2
L4 50 L1 AND L2
=> s l4 and l3
L5 24 L4 AND L3
=> d l5,cit,ab,1-24

1. 5,582,969, Dec. 10, 1996, **Mycobacteriophage** specific for the **mycobacterium** tuberculosis complex; Robert E. Pearson, et al., 435/5, 6, 7.91, 8, 172.1, 172.3, 320.1; 536/23.72 [IMAGE AVAILABLE]

US PAT NO: 5,582,969 [IMAGE AVAILABLE] L5: 1 of 24

ABSTRACT:
Mycobacteriophage DS6A has been characterized and found to specifically infect all species of the TB complex, without any detectable infection of **mycobacteria** species other than those of the TB complex. DNA sequence analysis revealed several potential open reading frames, including one encoding a protein analogous to gp37 of **mycobacteriophage** L5 and a second encoding a protein with significant homology to the S. coelicolor DNA polymerase .beta. subunit. Based on the DNA sequence analysis, cloning sites can be identified for insertion of reporter genes, making DS6A useful as a reporter phage for specific detection and identification of species of the TB complex.

2. 5,578,444, Nov. 26, 1996, Sequence-directed DNA-binding molecules compositions and methods; Cynthia A. Edwards, et al., 435/6, 7.23; 536/23.1; 935/76, 77 [IMAGE AVAILABLE]

US PAT NO: 5,578,444 [IMAGE AVAILABLE] L5: 2 of 24

ABSTRACT:
The present invention defines a DNA:protein-binding assay useful for screening libraries of synthetic or biological compounds for their ability to bind DNA test sequences. The assay is versatile in that any number of test sequences can be tested by placing the test sequence adjacent to a defined protein binding screening sequence. Binding of molecules to these test sequence changes the binding characteristics of the protein molecule to its cognate binding sequence. When such a molecule binds the test sequence the equilibrium of the DNA:protein complexes is disturbed, generating changes in the concentration of free DNA probe. Numerous exemplary target test sequences (SEQ ID NO:1 to SEQ

ID NO:600) are set forth. The assay of the present invention is also useful to characterize the preferred binding sequences of any selected DNA-binding molecule.

3. 5,574,138, Nov. 12, 1996, Epithelium-derived T-cell factor; Kenneth H. Grabstein, et al., 530/351; 424/85.2; 435/69.52 [IMAGE AVAILABLE]

US PAT NO: 5,574,138 [IMAGE AVAILABLE] L5: 3 of 24

ABSTRACT:
Nucleic acid sequences which encode biologically active ETF, expression vectors which direct the expression of ETF, ETF polypeptides, antibodies which specifically bind ETF and processes for preparing the same are disclosed. Also disclosed are methods for treating or preventing gastrointestinal diseases and HIV or HIV-associated diseases.

4. 5,573,910, Nov. 12, 1996, Detection of conversion to mucoidy in Pseudomonas aeruginosa infecting cystic fibrosis patients involving the algu gene; Vojo Deretic, et al., 435/6, 91.2; 536/22.1, 23.1, 24.3, 24.32 [IMAGE AVAILABLE]

US PAT NO: 5,573,910 [IMAGE AVAILABLE] L5: 4 of 24

ABSTRACT:
Compositions and methods for detecting the conversion to mucoidy in Pseudomonas aeruginosa are disclosed. Mucoidy is a critical P. aeruginosa virulence factor in cystic fibrosis that has been associated with biofilm develoment and resistance to phagocytosis. The present invention provides for detecting the switch from nonmucoid to mucoid state as caused by the interaction of the algU gene product, algU, with RNA polymerase. Inactivation of algU results in a loss of expression of genes, such as algD, dependent on algU for transcription. Also disclosed is a novel alginate biosynthesis heterologous expression system for use in screening candidate substances that inhibit conversion to mucoidy by inhibiting the interaction of algU with the RNA polymerase holoenzyme.

5. 5,550,040, Aug. 27, 1996, Method, reagents and kits for the detection of Neisseria gonorrhoeae; Ashok P. Purohit, et al., 435/91.2, 6, 91.1, 183, 810; 536/24.32, 24.33, 25.3; 935/76, 77, 78 [IMAGE AVAILABLE]

US PAT NO: 5,550,040 [IMAGE AVAILABLE] L5: 5 of 24

ABSTRACT:
Methods, reagents and kits are provided for simultaneously amplifying and detecting polynucleotide sequences in bacteria causing Neisseria gonorrhoeae and/or Chlamydia trachomatis using primers and probes specific for each bacterial species.

6. 5,547,834, Aug. 20, 1996, Recombinant CMV neutralizing proteins; Richard R. Spaete, et al., 435/5; 424/186.1, 230.1; 435/69.3, 172.1; 530/350; 935/65 [IMAGE AVAILABLE]

US PAT NO: 5,547,834 [IMAGE AVAILABLE] L5: 6 of 24

ABSTRACT:
The present invention provides recombinant polypeptides derived from CMV glycoprotein gB and truncated fragments thereof which contain at least one epitope which is immunologically identifiable with one encoded by the CMV genome. The complete characterization of the gB protein, including the identity of glycoprotein gp55, permits the production of polypeptides which are useful as standards or reagents in diagnostic tests and/or as components of vaccines. This invention provides recombinant polypeptides and recombinant polynucleotides encoding these polypeptides wherein a neutralizing epitope of gB is localized within gp55.

7. H 1,531, May 7, 1996, Thermophilic DNA polymerase; Ilse I. Blumentals, et al., 435/194 [IMAGE AVAILABLE]

US PAT NO: H 1,531 [IMAGE AVAILABLE] L5: 7 of 24

ABSTRACT:
The invention relates to a substantially pure thermostable DNA polymerase. Preferably, the DNA polymerase has a molecular weight of about 95 kilodaltons and is more thermostable than Taq DNA polymerase. The present invention also relates to cloning and expression of the DNA polymerase in E. coli, to DNA molecules containing the cloned gene, and to host cells which express said genes.

8. 5,494,810, Feb. 27, 1996, Thermostable ligase-mediated DNA amplifications system for the detection of genetic disease; Francis Barany, et al., 435/91.52, 4, 6, 91.2 [IMAGE AVAILABLE]

US PAT NO: 5,494,810 [IMAGE AVAILABLE] L5: 8 of 24

ABSTRACT:
The present invention relates to the cloning of the gene of a thermophilic DNA ligase, from Thermus aquaticus strain HB8, and the use of this ligase in a ligase chain reaction (LCR) assay for the detection of specific sequences of nucleotides in a variety of nucleic acid samples, and more particularly in those samples containing a DNA sequence characterized by a difference in the nucleic acid sequence from a standard sequence including single nucleic acid base pair changes, deletions, insertions or translocations.

9. 5,482,836, Jan. 9, 1996, DNA purification by triplex-affinity capture and affinity capture electrophoresis; Charles R. Cantor, et al., 435/6, 91.1; 536/23.1, 24.3, 24.33, 25.3, 25.32; 935/1, 2, 4, 16, 19, 76, 77 [IMAGE AVAILABLE]

US PAT NO: 5,482,836 [IMAGE AVAILABLE] L5: 9 of 24

ABSTRACT:
The invention provides a method for purifying or isolating double stranded DNA intact using triple helix formation. The method includes the steps of complexing an oligonucleotide and double stranded DNA to generate a triple helix and immobilization of the triple helix on a solid phase by means of a molecular recognition system such as avidin/biotin. The purified DNA is then recovered intact by treating the solid phase with a reagent that breaks the bonds between the oligonucleotide and the intact double stranded DNA while not affecting the Watson-Crick base pairs of the double helix. The present invention also provides a method for purifying or isolating double stranded DNA intact by complexing the double stranded DNA with a specific binding partner and recovering the complex during electrophoresis by immobilizing it on a solid phase trap imbedded in an electrophoretic gel.

10. 5,476,768, Dec. 19, 1995, **Mycobacteriophage** DSGA specific for the **mycobacterium** tuberculosis complex; Robert E. Pearson, et al., 435/6, 91.2; 536/22.1, 23.1, 24.32 [IMAGE AVAILABLE]

US PAT NO: 5,476,768 [IMAGE AVAILABLE] L5: 10 of 24

ABSTRACT:
Mycobacteriophage DS6A has been characterized and found to specifically infect all species of the TB complex, without any detectable infection of **mycobacteria** species other than those of the TB complex. DNA sequence analysis revealed several potential open reading frames, including one encoding a protein analogous to gp37 of **mycobacteriophage** L5 and a second encoding a protein with significant homology to the S. coelicolor DNA polymerase .beta. subunit. Based on the DNA sequence analysis, cloning sites can be identified for insertion of reporter genes, making DS6A useful as a reporter phage for specific detection and identification of species of the TB complex.

11. 5,470,718, Nov. 28, 1995, Equine herpesvirus type 1 glycoprotein D nucleic acids; Dennis J. O'3 Callaghan, 435/69.1, 5, 6, 172.3, 240.1, 252.3, 320.1; 536/22.1, 23.1; 935/6, 23, 66 [IMAGE AVAILABLE]

US PAT NO: 5,470,718 [IMAGE AVAILABLE] L5: 11 of 24

ABSTRACT:

The present invention is directed to a gene encoding an envelope glycoprotein of equine herpesvirus type 1 (EHV-1), the glycoprotein D (gD) gene, its gene product and antibodies directed against gD polypeptides. The envelope glycoproteins of herpesvirus are major targets of the immune response to herpesviral infection. Hence, an important aspect of this invention is directed towards a vaccine against EHV-1 and treatment of EHV-1 infection by anti-EHV-gD antibodies or antisera.

12. 5,468,634, Nov. 21, 1995, Axl oncogene; Edison T. Liu, 435/240.2, 6, 172.1, 252.3, 320.1; 436/64; 536/23.1, 23.5 [IMAGE AVAILABLE]

US PAT NO: 5,468,634 [IMAGE AVAILABLE] L5: 12 of 24

ABSTRACT:
Isolated DNA sequences encoding a mammalian axl receptor which exhibits axl oncogene activity are disclosed. Also disclosed are vectors containing such DNA sequences, host cells containing such DNA sequences, axl receptor proteins, and soluble axl receptors, chimeric proteins including the extracellular domain of the axl receptor and DNA sequences encoding such chimeric proteins, and antibodies which specifically bind the axl receptor.

13. 5,464,774, Nov. 7, 1995, Bovine basic fibroblast growth factor; Andrew J. Baird, et al., 536/23.51; 530/399 [IMAGE AVAILABLE]

US PAT NO: 5,464,774 [IMAGE AVAILABLE] L5: 13 of 24

ABSTRACT:
Substantially pure mammalian basic fibroblast growth factors are produced. The amino acid residue sequences of bovine and human bFGF are disclosed as well as a DNA chain encoding the polypeptide of the bovine species. By appropriately inserting a synthesized DNA chain into a cloning vector and using the cloning vector to transform cells, synthetic bovin bFGF can be obtained from transformed cell lines, both prokaryotic and eukaryotic.

14. 5,441,736, Aug. 15, 1995, Actinobacillus pleuropneumoniae outer membrane lipoprotein A and uses thereof; Gerald F. Gerlach, et al., 424/190.1, 256.1, 825; 530/350, 395 [IMAGE AVAILABLE]

US PAT NO: 5,441,736 [IMAGE AVAILABLE] L5: 14 of 24

ABSTRACT:
Novel vaccines for use against Actinobacillus pleuropneumoniae are disclosed. The vaccines contain at least one Actinobacillus pleuropneumoniae outer membrane lipoprotein A, or an immunogenic fragment thereof. Also disclosed are DNA sequences encoding these proteins,

vectors including these sequences and host cells transformed with these vectors. The vaccines can be used to treat or prevent porcine respiratory infections.

15. 5,434,073, Jul. 18, 1995, Fibrinolytic and anti-thrombotic cleavable dimers; Keith Dawson, et al., 435/216; 424/94.64; 435/69.7; 530/350, 402 [IMAGE AVAILABLE]

US PAT NO: 5,434,073 [IMAGE AVAILABLE] L5: 15 of 24

ABSTRACT:

Relatively inactive fusion proteins are activatable by enzymes of the clotting cascade to have fibrinolytic and/or clot formation inhibition activity. For example, a fusion protein comprising two hirudin or streptokinase molecules, linked by a cleavable linkage sequence, may be cleaved to yield anti-thrombotic hirudin or fibrinolytic streptokinase by thrombin or Factor Xa. Fibrinolytic or clot formation inhibition activity is therefore directed to the site of clot formation. Cleavable streptokinase/hirudin heterodimers are claimed.

16. 5,426,181, Jun. 20, 1995, DNA encoding cytokine-induced protein, TSG-14; Tae H. Lee, et al., 536/23.5; 435/69.1, 252.3, 320.1; 536/23.1 [IMAGE AVAILABLE]

US PAT NO: 5,426,181 [IMAGE AVAILABLE] L5: 16 of 24

ABSTRACT:
Pleiotropic pro-inflammatory cytokines, such as TNF and IL-1, induce expression of a polypeptide molecule, termed TSG-14, in connective tissue cells. The TSG-14 polypeptide and functional derivatives thereof, DNA coding therefor, expression vehicles, such as a plasmids, and host cells transformed or transfected with the DNA molecule, and methods for producing the polypeptide and the DNA are provided. Antibodies specific for the TSG-14 polypeptide are disclosed, as is a method for detecting the presence of TSG-14 polypeptide in a biological sample, using the antibody or another molecule capable of binding to TSG-14 such as hyaluronic acid. A method for detecting the presence of nucleic acid encoding a normal or mutant TSG-14 polypeptide, a method for measuring induction of expression of TSG-14 in a cell using either nucleic acid hybridization or immunoassay, a method for identifying a compound capable of inducing the expression of TSG-14 in a cell, and a method for measuring the ability of a cell to respond to TNF are also provided.

17. 5,422,242, Jun. 6, 1995, **Mycobacterium** primers and probes; Karen K. Y. Young, 435/6, 34; 536/24.3, 24.32, 24.33 [IMAGE AVAILABLE]

US PAT NO: 5,422,242 [IMAGE AVAILABLE] L5: 17 of 24

ABSTRACT:
Primers and probes can be used to detect nucleic acid from **Mycobacterium** in a sample and determine the species from which the nucleic acid originates. The primers amplify regions of the 16S ribosomal RNA gene and hybridize to regions conserved among species. Genus specific probes hybridize to sequences within the amplified region conserved among **mycobacterial** species, whereas the species specific probes hybridize to a variable region, so that the species identity can be uniquely determined. Consensus probes for detecting **mycobacteria** nucleic acids are provided which probes are not identical to any of the sequences of **mycobacterial** species.

18. 5,420,025, May 30, 1995, Recombinant transglutaminase; Hiroshi Takagi, et al., 435/193, 69.1, 252.3, 252.33, 252.35, 254.21; 536/23.2 [IMAGE AVAILABLE]

US PAT NO: 5,420,025 [IMAGE AVAILABLE] L5: 18 of 24

ABSTRACT:
A DNA gene which encodes transglutaminase, a plasmid in which the DNA gene is incorporated, a transformant transformed with the plasmid and a process for the production of transglutaminase that comprises culturing the transformant.

19. 5,411,886, May 2, 1995, Xylose isomerase gene of Thermus aquaticus; Shigezo Udaka, et al., 435/252.3, 233, 234, 252.31, 252.33, 252.35, 254.21, 320.1; 536/23.2, 23.7 [IMAGE AVAILABLE]

US PAT NO: 5,411,886 [IMAGE AVAILABLE] L5: 19 of 24

ABSTRACT:
A xylose isomerase gene from Thermus bacteria, such as Thermos aquaticus (ATCC 27634) and a gene having 60% or more of homology to the nucleotide sequence of Thermus aquaticus xylose isomerase gene of FIG. 1-3. A xylose isomerase from Thermus aquaticus characterized in that the xylose isomerase has the optimal pH of about 7, the stable pH range of from about 6 to 8.5, the optimal temperature of about 95.degree. C. and the molecular weight of about 44,000, and is stabilized with manganese or magnesium. A process for preparing a xylose isomerase comprising transforming a microorganism with a plasmid containing the above gene and a promoter, culturing the transformed microorganism and harvesting the produced xylose isomerase. A process for preparing fructose comprising isomerization of glucose to fructose in the presence of the above xylose isomerase.

20. 5,374,553, Dec. 20, 1994, DNA encoding a thermostable nucleic acid polymerase enzyme from thermotoga maritima; David H. Gelfand, et al., 435/252.3, 194, 252.33, 320.1; 536/23.2 [IMAGE AVAILABLE]

US PAT NO: 5,374,553 [IMAGE AVAILABLE] L5: 20 of 24

ABSTRACT:
A purified thermostable enzyme is derived from the eubacterium Thermotoga maritima. The enzyme has a molecular weight of about 97 kilodaltons and DNA polymerase I activity. The enzyme can be produced from native or recombinant host cells and can be used with primers and nucleoside triphosphates in a temperaturecycling chain reaction where at least one nucleic acid sequence is amplified in quantity from an existing sequence.

21. 5,356,796, Oct. 18, 1994, Repressor protein and operon for regulating expression of polypeptides and its use in the preparation of 2,2-dialkyglycine decarboxylase of Pseudomonas cepacia; John W. Keller, 435/69.1, 232, 252.3, 252.33, 320.1; 530/358; 536/23.7, 24.1; 935/11, 29, 33, 40, 43, 68, 72, 73 [IMAGE AVAILABLE]

US PAT NO: 5,356,796 [IMAGE AVAILABLE] L5: 21 of 24

ABSTRACT:
A nucleotide sequence coding for a repressor protein for regulating gene expression that comprises about a 687 bp nucleotide region beginning about 81 bases upstream from the 2,2-dialkylglycine decarboxylase structural gene shown in FIG. 3. The repressor protein comprises about 229 amino acids. The nucleotide sequence is useful for regulating gene expression in recombinant expression vectors. The vectors and E. coli cells transformed with the vectors are useful for preparing Pseudomonas cepacia 2,2-dialkylglycine decarboxylase.

22. 5,232,829, Aug. 3, 1993, Detection of chlamydia trachomatis by polymerase chain reaction using biotin labelled lina primers and capture probes; Mathew Longiaru, et al., 435/6, 29, 34, 35; 536/24.32, 24.33; 935/2, 16, 19 [IMAGE AVAILABLE]

US PAT NO: 5,232,829 [IMAGE AVAILABLE] L5: 22 of 24

ABSTRACT:
The present invention relates to the synthesis of amplified biotin-labelled DNA target sequences of Chlamydia trachomatis by polymerase chain reaction techniques and the detection of such sequences by a microtiter plate having plurality of wells and having bound thereto oligonucleotide capture probe complementary to said target sequence.

23. 5,210,025, May 11, 1993, Prepressor protein gene for regulating

expression of polypeptides and its use in the preparation of 2,2-dialkylglycine decarboxylase of Pseudomonas cepacia; John W. Keller, 435/69.1, 193, 252.33, 320.1; 536/23.2 [IMAGE AVAILABLE]

US PAT NO: 5,210,025 [IMAGE AVAILABLE] L5: 23 of 24

ABSTRACT:
A nucleotide sequence coding for a repressor protein for regulating gene expression comprises about a 687 bp nucleotide region beginning about 81 bases upstream from the 2,2-dialkylglycine decarboxylase structural gene shown in FIG. 3. The repressor protein comprises about 229 amino acids. The nucleotide sequence is useful for regulating gene expression in recombinant expression vectors. The vectors and E. coli cells transformed with the vectors are useful for preparing Pseudomonas cepacia 2,2-dialkylglycine decarboxylase.

24. 5,155,214, Oct. 13, 1992, Basic fibroblast growth factor; Andrew J. Baird, et al., 530/399; 435/69.4; 514/12 [IMAGE AVAILABLE]

US PAT NO: 5,155,214 [IMAGE AVAILABLE] L5: 24 of 24

ABSTRACT:
Substantially pure mammalian basic fibroblast growth factors are produced. The amino acid residue sequences of bovine and human bFGF are disclosed as well as a DNA chain encoding the polypeptide of the bovine species. By appropriately inserting a synthesized DNA chain into a cloning vector and using the cloning vector to transform cells, synthetic bFGF can be obtained from transformed cell lines, both prokaryotic and eukaryotic.
=>

8/3,AB/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08886349 94201349

Rapid and simple PCR assay for quantitation of human immunodeficiency virus type 1 RNA in plasma: application to acute retroviral infection.

Mulder J; McKinney N; Christopherson C; Sninsky J; Greenfield L; Kwok S
Department of Infectious Diseases, Roche Molecular Systems, Inc., Alameda, California 94501.

J Clin Microbiol (UNITED STATES) Feb 1994, 32 (2) p292-300, ISSN 0095-1137 Journal Code: HSH
Languages: ENGLISH
Document type: JOURNAL ARTICLE

A method for quantitating human immunodeficiency virus type 1 plasma viremia may be useful in monitoring disease progression and the responsiveness of patients to a therapeutic regimen or vaccine. A quantitative assay for viral RNA in plasma or sera that differs in several aspects from those reported previously was developed. First, whereas conventional reverse transcriptase-PCR assays involve a two-step process and use two enzymes, the method described uses a single enzyme, rTth DNA polymerase, for both reverse transcription and PCR. The reactions are carried out in a single tube and with a single buffer solution with uninterrupted thermal cycling. Second, uracil-N-glycosylase and dUTP are incorporated into the reaction mixtures to ensure that any carryover of DNA from previous amplifications will not compromise quantitation. Third, a quantitation standard is incorporated into each reaction mixture so that differences in amplification efficiency caused by sample interferents, variability in reaction conditions, or thermal cycling can be normalized. To ensure comparable amplification efficiency, the quantitation standard has the same primer-binding regions as the human immunodeficiency virus type 1 target and generates an amplified product of the same size and base composition. The probe-binding region was replaced with a sequence that can be detected separately. Fourth, a colorimetric detection format was modified to provide at least a four-log-unit dynamic range. The quantitative assay requires only a single amplification of the sample and can be completed in less than 8 h. The procedure was used on archival samples to demonstrate the viremic spike in acute infection and the suppressed levels of circulating virus following seroconversion.

12/3,AB/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09691525 96213125

Analysis of RNA polymerase gene mutation in three isolates of rifampicin resistant Mycobacterium tuberculosis.

Vattanaviboon P; Sukchawalit R; Jearanaikoon P; Chuchottaworn C; Ponglikitmongkol M

Department of Biochemistry, Faculty of Science, Mahidol University, Bangkok, Thailand.

Southeast Asian J Trop Med Public Health (THAILAND) 1995, 26 Suppl 1 p333-6, ISSN 0038-3619 Journal Code: UVN

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Drug resistance in tuberculosis (TB) has become a major public health threat, particularly when the disease cannot be 100% controlled by BCG vaccination. In Thailand, resistance to rifampicin, a major component of multidrug regimens of treatment, is the common cause of tuberculosis recurrence. The mechanism of rifampicin resistance involves alterations of the RNA polymerase subunit beta (rpo B) gene. Mutations in rpo B gene were often found to cluster within a region of 23 amino acids starting from amino acid residue 511 to residue 533. Direct PCR sequencing was utilized to compare base changes in rpo B gene in three rifampicin resistant phenotypes of M. tuberculosis isolated from Thai patients. The sequences showed one base substitution at codon 531 resulting in an amino acid change from serine (TCG) to leucine (TTG) in a multidrug resistant isolate compared to that of a sensitive isolate, whereas a point mutation at codon 516 causing a change from aspartic acid (GAC) to tyrosine (TAC) was detected in a multidrug resistant isolate from a HIV positive patient. In an isolate resistant only to rifampicin a double mutation at codon 531 changing serine (TCG) to phenylalanine (TTT) was found. No mutations were observed in the same region in streptomycin, ethambutol or isoniazid resistant isolates. This finding reports two new types of mutation (GAC to TAC at codon 516 and TCG to TTT at codon 531) and confirms a direct correlation between rpo B gene alteration and rifampicin resistant phenotype in M. tuberculosis.

Set	Items	Description
S1	11585	(CLEAVASE BN) OR (THERMUS AQUATICUS) OR TAC OR (THERMUS THERMOPHILUS) OR TTH OR (EXO III) OR RAD1/RAD10
S2	1127716	VIRAL? OR VIRUS
S3	929402	MYCOBACTER? OR CAMPYLOBACTER OR ESCHERICHIA OR (E. COLI) OR SALMONELLA OR SHIGELLA OR STAPH?
S4	20101	MULTIDRUG
S5	949	S1 AND S2
S6	2186	(7(W)DEAZA(W)DATP) OR (7(W)DEAZA(W)DGTP) OR DUTP
S7	2	S5 AND S6
S8	2	RD (unique items)
S9	2210	S3 AND S4
S10	1	S9 AND S6
S11	0	C7DADTP OR C7DGDTP
S12	2	S9 AND S1

?

11/3,AB/1 (Item 1 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

11727881 BIOSIS Number: 98327881
Rapid genotyping of hepatitis C virus isolates by dideoxy fingerprinting
Fox S A; Lareu R R; Swanson N R
Mol. Hepatol., Univ. Dep. Med., Dep. Gastroenterol., Sir Charles Gairdner Hosp., Perth, WA 6009, Australia
Journal of Virological Methods 53 (1). 1995. 1-9.
Full Journal Title: Journal of Virological Methods
ISSN: 0166-0934
Language: ENGLISH
Print Number: Biological Abstracts Vol. 100 Iss. 003 Ref. 035605
A number of distinct hepatitis C virus (HCV) types and subtypes have been identified by DNA sequencing of multiple genome regions. It has been postulated that these might also reflect phenotypic differences in the nature of HCV infection. Recent evidence suggests a relationship between HCV genotype and alpha-interferon response in patients with chronic hepatitis C. A simplified method of genotyping in comparison to direct DNA sequencing was investigated with the intention of providing a rapid, less labour-intensive method for routine genotyping. HCV RNA was extracted from serum by a modified guanidinium/acid-phenol extraction and peripheral blood lymphocytes using RNAzol B (Cinna-Biotecx). The RNA was reverse transcribed and a 287 hp segment of the 5' non-coding region (5' NCR) amplified using a nested-PCR reaction. PCR products were purified using Qiaquick spin columns. Products were directly sequenced by cycle sequencing. Dideoxy termination analysis was carried out by cyclic extension of a 33P-labelled primer by Tth polymerase with termination by dideoxy thiamine (ddT) or cytosine (ddC). Reaction products were analysed by electrophoresis on denaturing 7 M urea/6% acrylamide gels followed by autoradiography. Computer aided sequence analysis indicated that conserved 5' NCR sequence variation alone was sufficient to identify HCV types 1a, 1b, 2a, 2b, 3 and 4. Dideoxy fingerprinting improved greatly the efficiency of genotyping with an approximate four-fold increase in throughput. In addition, the results were very easily analysed although it was essential to run appropriate controls for each genotype. Reactions incorporating ddT distinguished types 1, 2a, 2b, 3 (provisionally 1a & 1b); a ddC reaction confirmed 1a and 1b typing. Standard denaturing gels gave superior results than a variety of non-denaturing ('SSCP') gels. Our results show that dideoxy fingerprinting is a reliable and efficient alternative to direct sequencing for HCV genotyping which is adaptable to semi-routine screening.

11/3,AB/2 (Item 2 from file: 5)
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

11571775 BIOSIS Number: 98171775

Effective production of the hepatitis C virus core antigen having high purity in Escherichia coli

Seki M; Honda Y; Kondo J; Fukuda K; Ohta K; Sugimoto J; Yamada E

Biosci. Lab., Res. Cent., Mitsubishi Kasei Corp., 1000 Kamoshida-cho, Midori-ku, Yokohama 227, Japan

Journal of Biotechnology 38 (3). 1995. 229-241.

Full Journal Title: Journal of Biotechnology

ISSN: 0168-1656

Language: ENGLISH

Print Number: Biological Abstracts Vol. 099 Iss. 008 Ref. 112078

The amino-terminal half of putative nucleocapsid (core) protein (amino acids 1-115) of hepatitis C virus (HCV) was directly overproduced in Escherichia coli under the control of the tac promoter. Overproduction of core antigen was achieved by inserting several target genes and by optimizing the culture conditions, whereas a large amount of directly expressed and purified core antigen has not yet been reported. Although the level of expression was comparable to that of the conventional E. coli fused expression system, our recombinant proteins contain only HCV amino acid sequence. Using recombinant E. coli, overproduced large-scale culture system was achieved in jar-fermenter. A highly purified sample of the expressed protein was obtained by ion-exchange and gel permeation column chromatography in the presence of 8 M urea. From a 3.5 1 culture, apprx 440 mg of recombinant core protein was obtained after a two-step purification procedure. An enzyme-linked immunosorbent assay developed using the highly purified antigen satisfactorily diagnosed hepatitis C.

11/3,AB/3 (Item 3 from file: 5)

DIALOG(R)File 5:BIOSIS PREVIEWS(R)

11519050 BIOSIS Number: 98119050

Different cellular patterns associated with hepatitis C virus reactivation, cytomegalovirus infection, and acute rejection in liver transplant patients monitored with transplant aspiration cytology

Lautenschlager I; Nashan B; Schlitt H-J; Hoshino K; Ringe B; Tillmann H L ; Manns M; Wonigeit K; Pichlmayr R

Transplantation Lab., Helsinki Univ. Central Hosp., P.O. Box 21, SF-00014 Univ. Helsinki, Finland

Transplantation (Baltimore) 58 (12). 1994. 1339-1345.

Full Journal Title: Transplantation (Baltimore)

ISSN: 0041-1337

Language: ENGLISH

Print Number: Biological Abstracts Vol. 099 Iss. 006 Ref. 075607

Fine-needle aspiration biopsy (FNAB) is a routine diagnostic tool used for the monitoring of the graft during the first postoperative weeks after liver transplantation. The cellular pattern of acute liver rejection is typical in transplant aspiration cytology (TAC), documented and published by several authors. The lymphoid response associated with various viral infections may, however, provide differential diagnostic problems in the cytological monitoring. In this study, we have investigated in detail the cellular pattern of lymphoid response associated with hepatitis C virus (HCV) reactivation, and compared it with the pattern of cytomegalovirus (CMV) infection and with the typical diagnostic findings of acute cellular rejection. HCV reactivation was associated with rather mild total inflammation in the graft (4.5 +- 1.5 CIU at the peak). The inflammatory infiltrate consisted mainly of small lymphocytes (3.1 +- 0.2 CIU at the peak), with only occasional activated cells and without lymphoid blast response. No lymphoid activation was seen in the blood. CMV infection was associated with a mild immune response (3.9 +- 0.4 CIU at the peak) recorded as a slight lymphoid activation and occasional blast cells both in blood and in the graft together with lymphocytosis in the graft (2.4 +- 0.7 CIU at the peak). The typical findings of acute rejection were easily distinguished from the cellular pictures of both viral infections. The rejections were lymphoid blast (3.6 +- 3.4 CIU at the peak) and activated lymphocyte (3.5 +- 2ds
.6 at the peak), dominated by a high peak of total
inflammation (9.3 +- 7.0 CIU). No blast cells and only a few activated cells were seen in the blood during rejection episodes. Thus, the cellular patterns of HCV reactivation and CMV infection differed slightly from each other, but significantly from that of acute liver allograft rejection monitored with the FNAB cytology.

10132573 BIOSIS Number: 95132573

DETECTION OF HEPATITIS C VIRUS RNA BY A COMBINED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION ASSAY

YOUNG K K Y; RESNICK R M; MYERS T W

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J CLIN MICROBIOL 31 (4). 1993. 882-886. CODEN: JCMID

Full Journal Title: Journal of Clinical Microbiology

Language: ENGLISH

Amplification of RNA by the polymerase chain reaction (PCR) is normally a two-step process requiring separate enzymes and buffer conditions. We describe a combined reverse transcription-PCR (RT-PCR) assay for hepatitis C virus (HCV) RNA amplification in which a single enzyme and buffer

condition are used. In this assay, both the RT and PCR steps are carried out with the thermoactive DNA polymerase of Thermus thermophilus. A transcription vector containing HCV sequences has also been constructed to generate quantifiable HCV RNA templates that can be used to optimize reaction conditions and to assess the efficiency of amplification. Amplification from .ltoreq. 100 copies of RNA was detected reproducibly by gel electrophoresis. The assay sensitivity was increased to 10 RNA copies by hybridization to a probe. The patterns of viremia in three individuals infected with HCV were examined by amplification of HCV RNA from plasma samples collected serially over a period of 1 year. These results were correlated with the times of seroconversion and the onset of rise in levels of alanine aminotransferase in serum. In all three subjects, HCV RNA was detected prior to seroconversion and the initial rise in levels of alanine aminotransferase in serum. Upon seroconversion, HCV RNA fell to a level below the detection limit of the assay. This pattern of transient viremia appears to be characteristic of acute, resolving HCV infections. The combined RT-PCR assay is a sensitive method which circumvents the problems associated with PCR amplification of RNA. Using this assay, we demonstrated that three donors infected by the same index case all have similar patterns of viremia.

11/3,AB/5 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09492728 96014328
Reverse transcription combined with polymerase chain reaction as a detection method for pestiviral infections.
Stadejek T; Pejsak Z; Kwinkowski M; Okruszek A; Winiarczyk S
Department of Swine Diseases, National Veterinary Research Institute, Pulawy, Poland.
Rev Sci Tech (FRANCE) Sep 1995, 14 (3) p811-8, ISSN 0253-1933
Journal Code: A9R
Languages: ENGLISH
Document type: JOURNAL ARTICLE
An assay based on reverse transcription coupled with the polymerase chain reaction (RT-PCR) was used for the detection of hog cholera virus (HCV) and bovine virus diarrhoea virus (BVDV) in cell culture. In this study, a precipitate of the supernatants derived from cell cultures infected with HCV and BVDV was used in RT reactions, in place of extracted viral RNA. Both RT and PCR were performed using recombinant Thermus thermophilus (rTth) DNA polymerase. The specificity of the RT-PCR products was confirmed by hybridisation with a digoxygenin-labelled DNA probe. The results not only show that the stage of RNA isolation can be bypassed, but also illustrate an easy and efficient means of obtaining templates suitable for identification and characterisation of HCV and BVDV in tissue culture by

RT-PCR.

11/3,AB/6 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

200862 DBA Accession No.: 96-11633
Construction, purification and immunogenicity of antigen-antibody-LTB complexes - Escherichia coli heat-labile enterotoxin B-subunit and epitope affinity tail fusion protein expression in Vibrio sp., for SIV virus recombinant vaccine-antibody complex production
AUTHOR: Green E A; Botting C; Webb H M; Hirst T R; +Randall R E
CORPORATE AFFILIATE: Univ.St.Andrews Univ.Kent
CORPORATE SOURCE: School of Biological and Medical Sciences, The Irvine Building, North Street, University of St. Andrews, Fife KY16 9AL, UK.
JOURNAL: Vaccine (14, 10, 949-58) 1996
ISSN: 0264-410X CODEN: VACCDE
LANGUAGE: English
ABSTRACT: An oligonucleotide encoding a short epitope peptide tag (Pk) was inserted at the 3'-end of a gene encoding the B-subunit of Escherichia coli heat-labile enterotoxin (LTB), and the fusion protein was expressed in E. coli and Vibrio sp. 60 under the control of a tac promoter using plasmid pTRH101R as a vector (to give plasmid pTRH-Pk). Expression of LTB-Pk in Vibrio sp. reached 6-12 mg/l medium (after 6-12 hr induction). The protein was purified by cation-exchange chromatography. The presence of the Pk epitope on LTB-Pk was used to construct novel macromolecular complexes containing LTB-Pk, an anti-Pk monoclonal antibody (SV5-P-k) and Pk-linked recombinant SIV virus proteins. These complexes were highly immunogenic in mice, inducing both humoral and cell-mediated responses to the recombinant SIV antigens. (41 ref)

11/3,AB/7 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

198633 DBA Accession No.: 96-09404 PATENT
Cleavage of nucleic acids to detect mutation - using a nuclease to detect a DNA polymorphism in a human p53 gene or a microorganism 16S ribosome RNA gene, for cancer diagnosis or strain identification
AUTHOR: Dahlberg J E; Lyamichev V I; Brow M A D; Oldenburg M C; Heisler L M; Fors L; Olive D M
CORPORATE SOURCE: Madison, WI, USA.
PATENT ASSIGNEE: Third-Wave-Technol. 1996
PATENT NUMBER: WO 9615267 PATENT DATE: 960523 WPI ACCESSION NO.:

96-259862 (9626)
PRIORITY APPLIC. NO.: US 520946 APPLIC. DATE: 950830
NATIONAL APPLIC. NO.: WO 95US14673 APPLIC. DATE: 951109
LANGUAGE: English
ABSTRACT: A new method for treating a nucleic acid substrate (e.g. an oligonucleotide analog) involves cleavage with an enzyme (preferably a nuclease, e.g. Cleavase-BN, Thermus aquaticus DNA-polymerase (EC-2.7.7.7), Thermus thermophilus DNA-polymerase, Escherichia coli exonuclease-III or Saccharomyces cerevisiae Rad1/Rad10 complex). The oligonucleotide analog may contain 7-deaza-dATP, 7-deaza-dGTP or dUTP, and may be ss or ds DNA or RNA. Ds nucleic acid may be converted to ss form, e.g. by heat denaturation, and induced to form a secondary structure. The substrate may contain a human p53 gene or 16S ribosome RNA gene sequence. The enzyme may be introduced in a solution containing manganese, followed by heat treatment, cleavage structure formation at reduced temp., reaction with the enzyme, and product detection and comparison with a reference sequence. The method may be used in p53 mutation detection or identification of a microorganism strain, e.g. Campylobacter, Escherichia, multidrug-resistant Mycobacterium tuberculosis, Salmonella, Shigella, Staphylococcus, hepatitis C virus or SIV virus. (433pp)

11/3,AB/8 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

136056 DBA Accession No.: 92-08548
Cloning, expression, and mutagenesis of SIVmac proteinase in E. coli - SIV virus recombinant protease production in Escherichia coli (conference abstract)
AUTHOR: Corr B R; Richardson M; Wilderspin A F
CORPORATE AFFILIATE: Brit.Bio-technol.
CORPORATE SOURCE: Laboratory of Molecular Biology, Department of Crystallography, Birkbeck College, Malet Street, London, WC1E 7HX, UK.
JOURNAL: Biochem.Soc.Trans. (20, 2, 160S) 1992
CODEN: 9996F
LANGUAGE: English
ABSTRACT: In order to evaluate the degree of functional homology of HIV virus-1/-2 aspartic protease (AP) and SIV virus (SIVmac) AP, AP was produced in Escherichia coli. The AP gene (encoding SIVmac AP, the transframe protein and the first 25 amino acids of reverse-transcriptase (EC-2.7.7.49)) was cloned under the control of the tac promoter in plasmid pGEX-2T to give plasmid pGP-2T or in plasmid pGEX-3X to give plasmid pGP-3X. Both vectors were expressed in E. coli TG1 and produced soluble AP. The SIVmac AP gene was also inserted into plasmid pSD18 (containing the horseradish peroxidase

(HRP, EC-1.11.1.7) gene) to yield plasmid pOGS445. E. coli HW1110 containing this plasmid produced 54 kDa insoluble HRP-AP-HRP fusion protein in inclusion bodies (IBs). The HRP-AP-HRP construct was cloned into plasmid pJLA503 to give plasmid pOGS457 (containing the phage lambda pR/pL promoter). This plasmid was expressed in E. coli HW87, and insoluble AP was formed in IBs. All cultures were grown at 37 deg, and AP was induced by IPTG or by heat shock. Soluble AP retarded cell growth, while insoluble AP did not. Plasmid pOGS457 gave the highest expression levels. (8 ref)

11/3,AB/9 (Item 4 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

115450 DBA Accession No.: 91-03092 PATENT
New oligonucleotide primer specific for HIV virus-2 or SIV virus mac - DNA primer useful in genome amplification of virus nucleic acid before detection by hybridization; potential disease diagnosis
PATENT ASSIGNEE: Inst.Pasteur; INSERM 1990
PATENT NUMBER: WO 9015158 PATENT DATE: 901213 WPI ACCESSION NO.: 91-007227 (9101)
PRIORITY APPLIC. NO.: FR 897355 APPLIC. DATE: 890602
NATIONAL APPLIC. NO.: WO 90FR394 APPLIC. DATE: 900605
LANGUAGE: French
ABSTRACT: An oligonucleotide primer of 15-25 nucleotides, which is useful for genome amplification of HIV virus-2 ROD and SIV virus mac 142, is claimed. The DNA primers are useful for in vitro diagnosis of infections caused by all strains of HIV virus-2 and SIV virus. The DNA probe is preferably LTR1 (GGT TCT CTC CAG CAC TAG CAG G), LTR2 (GGT CCT AAC AGA CCA GGG TC), GAG1 (ATG GGC GCG AGA AAC TCC GTC TTG), GAG5 (ATG GTG CTG TTG GTC TAC TTG T), GAG2 (CCC GGC GGA AAG AAA AAG TAC A), GAG2B (TGT ACT TTT TCT TTC CGC CGG G), POL1 (TGG GGA AAG AAG CCC CGC AA), POL2 (CCA AAG AGA GAA TTG AGG TGC AGC), P1 (CAG AAA TAG GGA TAC TTG GGG AAC C), P2 (GCC TGA ATA ATT GGT ATC ATT ACA), P2B (TGT AAT GAT ACC AAT TAT TCA GGC), P4 (AGT TCT GCC ACC TGT GCA CTA AAG G), P6 (GGG ATA GTG CAG CAA CAG CAA CAG), P7 (CAT TTC CTG ATC CGC CAG CTG AT), P7B (ATC AGC TGG CGG ATC AGG AAA TG) or P8 (GCA GGG AAC ACC CAG GCT CTA C). Immunogenic compositions contain a pharmaceutically acceptable vehicle and recombinant proteins, which are prepared by expressing DNA sequences, which have been amplified by the DNA primer, in a host. A method for hybridizing a sample to the DNA probe is described. (31pp)

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Set	Items	Description
S1	9984	(CLEAVASE BN) OR (THERMUS ACQUATICUS) OR TAC OR TTH OR (THERMUS THERMOPILUS) OR EXO III OR RAD1/RAD10

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S2          5787   CHV OR (HEPATITUS C) OR SIV OR (SIMIAN IMMUNODEF?)
S3         22033   HCV OR (HEPATITIS C)
S4          2833   THERMUS(W)THERMOP?
S5             1   CLEAVASE(W)BN
S6             5   THERMUS(W)ACQUATI?
S7            15   CLEAVASE
S8         12742   S1 OR S4 OR S6 OR S7
S9         27816   S2 OR S3
S10           17   S8 AND S9
S11            9   RD (unique items)
?
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